

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Rauch, Charles  
Walczak, Henning
- (ii) TITLE OF INVENTION: Receptor That Binds TRAIL
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
  - (B) STREET: 51 University Street
  - (C) CITY: Seattle,
  - (D) STATE: WA
  - (E) COUNTRY: US
  - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: Apple Power Macintosh
  - (C) OPERATING SYSTEM: Macintosh 7.6
  - (D) SOFTWARE: Microsoft Word, Version 6.0.1
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US --to be assigned--
  - (B) FILING DATE: 20-AUG-1999
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/883,036
  - (B) FILING DATE: 26-JUN-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/869,852
  - (B) FILING DATE: 04-JUN-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/829,536
  - (B) FILING DATE: 28-MAR-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/815,255
  - (B) FILING DATE: 12-MAR-1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/799,861
  - (B) FILING DATE: 13-FEB-1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Anderson, Kathryn A.
  - (B) REGISTRATION NUMBER: 32,172
  - (C) REFERENCE/DOCKET NUMBER: 2625-E
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (206) 587-0430
  - (B) TELEFAX: (206) 233-0644
  - (C) TELEX: 756822

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1323 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: huTrail-R

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..1323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG	GAA	CAA	CGG	GGA	CAG	AAC	GCC	CCG	GCC	GCT	TCG	GGG	GCC	CGG	AAA	48
Met	Glu	Gln	Arg	Gly	Gln	Asn	Ala	Pro	Ala	Ala	Ser	Gly	Ala	Arg	Lys	
1				5					10					15		
AGG	CAC	GGC	CCA	GGA	CCC	AGG	GAG	GCG	CGG	GGA	GCC	AGG	CCT	GGG	CCC	96
Arg	His	Gly	Pro	Gly	Pro	Arg	Glu	Ala	Arg	Gly	Ala	Arg	Pro	Gly	Pro	
			20					25					30			
CGG	GTC	CCC	AAG	ACC	CTT	GTG	CTC	GTT	GTC	GCC	GCG	GTC	CTG	CTG	TTG	144
Arg	Val	Pro	Lys	Thr	Leu	Val	Leu	Val	Val	Ala	Ala	Val	Leu	Leu	Leu	
		35				40						45				
GTC	TCA	GCT	GAG	TCT	GCT	CTG	ATC	ACC	CAA	CAA	GAC	CTA	GCT	CCC	CAG	192
Val	Ser	Ala	Glu	Ser	Ala	Leu	Ile	Thr	Gln	Gln	Asp	Leu	Ala	Pro	Gln	
	50					55					60					
CAG	AGA	GCG	GCC	CCA	CAA	CAA	AAG	AGG	TCC	AGC	CCC	TCA	GAG	GGA	TTG	240
Gln	Arg	Ala	Ala	Pro	Gln	Gln	Lys	Arg	Ser	Ser	Pro	Ser	Glu	Gly	Leu	
65				70						75					80	
TGT	CCA	CCT	GGA	CAC	CAT	ATC	TCA	GAA	GAC	GGT	AGA	GAT	TGC	ATC	TCC	288
Cys	Pro	Pro	Gly	His	His	Ile	Ser	Glu	Asp	Gly	Arg	Asp	Cys	Ile	Ser	
			85						90					95		
TGC	AAA	TAT	GGA	CAG	GAC	TAT	AGC	ACT	CAC	TGG	AAT	GAC	CTC	CTT	TTC	336
Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr	His	Trp	Asn	Asp	Leu	Leu	Phe	
			100					105					110			
TGC	TTG	CGC	TGC	ACC	AGG	TGT	GAT	TCA	GGT	GAA	GTG	GAG	CTA	AGT	CCG	384
Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	
		115					120					125				
TGC	ACC	ACG	ACC	AGA	AAC	ACA	GTG	TGT	CAG	TGC	GAA	GAA	GGC	ACC	TTC	432
Cys	Thr	Thr	Thr	Arg	Asn	Thr	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	
	130					135					140					
CGG	GAA	GAA	GAT	TCT	CCT	GAG	ATG	TGC	CGG	AAG	TGC	CGC	ACA	GGG	TGT	480
Arg	Glu	Glu	Asp	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys	
145					150					155					160	
CCC	AGA	GGG	ATG	GTC	AAG	GTC	GGT	GAT	TGT	ACA	CCC	TGG	AGT	GAC	ATC	528
Pro	Arg	Gly	Met	Val	Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	
				165					170					175		

GAA Glu	TGT Cys	GTC Val	CAC His 180	AAA Lys	GAA Glu	TCA Ser	GGT Gly	ACA Thr 185	AAG Lys	CAC His	AGT Ser	GGG Gly	GAA Glu 190	GCC Ala	CCA Pro	576
GCT Ala	GTG Val	GAG Glu 195	GAG Glu	ACG Thr	GTG Val	ACC Thr	TCC Ser 200	AGC Ser	CCA Pro	GGG Gly	ACT Thr	CCT Pro 205	GCC Ala	TCT Ser	CCC Pro	624
TGT Cys	TCT Ser 210	CTC Leu	TCA Ser	GGC Gly	ATC Ile	ATC Ile 215	ATA Ile	GGA Gly	GTC Val	ACA Thr	GTT Val 220	GCA Ala	GCC Ala	GTA Val	GTC Val	672
TTG Leu 225	ATT Ile	GTG Val	GCT Ala	GTG Val	TTT Phe 230	GTT Val	TGC Cys	AAG Lys	TCT Ser	TTA Leu 235	CTG Leu	TGG Trp	AAG Lys	AAA Lys	GTC Val 240	720
CTT Leu	CCT Pro	TAC Tyr	CTG Leu	AAA Lys 245	GGC Gly	ATC Ile	TGC Cys	TCA Ser	GGT Gly 250	GGT Gly	GGT Gly	GGG Gly	GAC Asp	CCT Pro 255	GAG Glu	768
CGT Arg	GTG Val	GAC Asp	AGA Arg 260	AGC Ser	TCA Ser	CAA Gln	CGA Arg	CCT Pro 265	GGG Gly	GCT Ala	GAG Glu	GAC Asp	AAT Asn 270	GTC Val	CTC Leu	816
AAT Asn	GAG Glu	ATC Ile 275	GTG Val	AGT Ser	ATC Ile	TTG Leu	CAG Gln 280	CCC Pro	ACC Thr	CAG Gln	GTC Val	CCT Pro 285	GAG Glu	CAG Gln	GAA Glu	864
ATG Met	GAA Glu 290	GTC Val	CAG Gln	GAG Glu	CCA Pro	GCA Ala 295	GAG Glu	CCA Pro	ACA Thr	GGT Gly	GTC Val 300	AAC Asn	ATG Met	TTG Leu	TCC Ser	912
CCC Pro 305	GGG Gly	GAG Glu	TCA Ser	GAG Glu	CAT His 310	CTG Leu	CTG Leu	GAA Glu	CCG Pro	GCA Ala 315	GAA Glu	GCT Ala	GAA Glu	AGG Arg	TCT Ser 320	960
CAG Gln	AGG Arg	AGG Arg	AGG Arg	CTG Leu 325	CTG Leu	GTT Val	CCA Pro	GCA Ala	AAT Asn 330	GAA Glu	GGT Gly	GAT Asp	CCC Pro	ACT Thr 335	GAG Glu	1008
ACT Thr	CTG Leu	AGA Arg	CAG Gln 340	TGC Cys	TTC Phe	GAT Asp	GAC Asp	TTT Phe 345	GCA Ala	GAC Asp	TTG Leu	GTG Val	CCC Pro 350	TTT Phe	GAC Asp	1056
TCC Ser	TGG Trp	GAG Glu 355	CCG Pro	CTC Leu	ATG Met	AGG Arg	AAG Lys 360	TTG Leu	GGC Gly	CTC Leu	ATG Met	GAC Asp 365	AAT Asn	GAG Glu	ATA Ile	1104
AAG Lys	GTG Val 370	GCT Ala	AAA Lys	GCT Ala	GAG Glu	GCA Ala 375	GCG Ala	GGC Gly	CAC His	AGG Arg	GAC Asp 380	ACC Thr	TTG Leu	TAC Tyr	ACG Thr	1152
ATG Met 385	CTG Leu	ATA Ile	AAG Lys	TGG Trp	GTC Val 390	AAC Asn	AAA Lys	ACC Thr	GGG Gly	CGA Arg 395	GAT Asp	GCC Ala	TCT Ser	GTC Val	CAC His 400	1200
ACC Thr	CTG Leu	CTG Leu	GAT Asp	GCC Ala 405	TTG Leu	GAG Glu	ACG Thr	CTG Leu	GGA Gly 410	GAG Glu	AGA Arg	CTT Leu	GCC Ala	AAG Lys 415	CAG Gln	1248
AAG Lys	ATT Ile	GAG Glu	GAC Asp 420	CAC His	TTG Leu	TTG Leu	AGC Ser	TCT Ser 425	GGA Gly	AAG Lys	TTC Phe	ATG Met	TAT Tyr 430	CTA Leu	GAA Glu	1296



Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu  
 260 265 270  
 Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu  
 275 280 285  
 Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser  
 290 295 300  
 Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser  
 305 310 315 320  
 Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp Pro Thr Glu  
 325 330 335  
 Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp  
 340 345 350  
 Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile  
 355 360 365  
 Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr  
 370 375 380  
 Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His  
 385 390 395 400  
 Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln  
 405 410 415  
 Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu  
 420 425 430  
 Gly Asn Ala Asp Ser Ala Met Ser \*  
 435 440

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 157 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: internal
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: huTrail-R frag
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 3..155
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CT GAG ACT CTG AGA CAG TGC TTC GAT GAC TTT GCA GAC TTG GTG CCC 47  
 Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro 15  
 1 5 10

TTT GAC TCC TGG GAG CCG CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT 95  
 Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn 30  
 20 25

GAG ATA AAG GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 143  
 Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu 45  
 35 40

TNC ACN ATG CTG AT 157  
 Xaa Thr Met Leu 50

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 51 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe 15  
 1 5 10

Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu 30  
 20 25

Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Xaa 45  
 35 40

Thr Met Leu 50

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: FLAG peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Tyr Lys Asp Asp Asp Asp Lys 5  
 1